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## FIG. 1A

```

5'   11      20      29      38      47      56
GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT
-----
      65      74      83      92     101     110
ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA
-----
      M   E   S   R   K   D   I   T   N   Q   E   E   L   W   K

      119     128     137     146     155     164
ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA
-----
      M   K   P   R   R   N   L   E   E   D   D   Y   L   H   K   D   T   G

      173     182     191     200     209     218
GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT
-----
      E   T   S   M   L   K   R   P   V   L   L   H   L   H   Q   T   A   H

      227     236     245     254     263     272
GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA
-----
      A   D   E   F   D   C   P   S   E   L   Q   H   T   Q   E   L   F   P

      281     290     299     308     317     326
CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT
-----
      Q   W   H   L   P   I   K   I   A   A   I   I   A   S   L   T   F   L

      335     344     353     362     371     380
TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT
-----
      Y   T   L   L   R   E   V   I   H   P   L   A   T   S   H   Q   Q   Y

      389     398     407     416     425     434
TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC
-----
      F   Y   K   I   P   I   L   V   I   N   K   V   L   P   M   V   S   I

      443     452     461     470     479     488
ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT
-----
      T   L   L   A   L   V   Y   L   P   G   V   I   A   A   I   V   Q   L

      497     506     515     524     533     542
CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA
-----
      H   N   G   T   K   Y   K   K   F   P   H   W   L   D   K   W   M   L

      551     560     569     578     587     596
ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT
-----
      T   R   K   Q   F   G   L   L   S   F   F   F   A   V   L   H   A   I

      605     614     623     632     641     650
TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG
-----
      Y   S   L   S   Y   P   M   R   R   S   Y   R   Y   K   L   L   N   W

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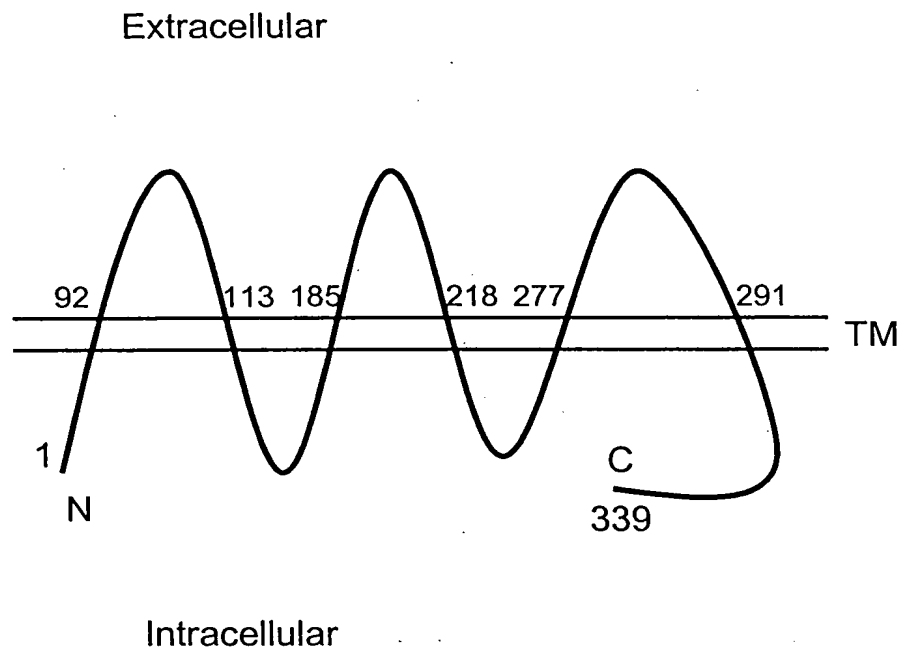
659	668	677	686	695	704
GCA TAT CAA CAG GTC	CAA CAA AAT	AAA GAA GAT	GCC TGG ATT	GAG CAT GAT	GTT
A Y Q Q V	Q Q N	K E D	A W I	E H D	V
713	722	731	740	749	758
TGG AGA ATG GAG ATT	TAT GTG TCT	CTG GGA ATT	GTG GGA TTG	GCA ATA CTG	GCT
W R M E I	Y V S	L G I	V G L	A I L	A
767	776	785	794	803	812
CTG TTG GCT GTG ACA TCT	ATT CCA TCT	GTG AGT GAC	TCT TTG ACA	TGG AGA	GAA
L L A V T	S I P	S V S	D S L	T W R	E
821	830	839	848	857	866
TTT CAC TAT ATT CAG	AGC AAG CTA	GGA ATT GTT	TCC CTT CTA	CTG GGC ACA	ATA
F H Y I Q	S K L	G I V	S L L	L G T	I
875	884	893	902	911	920
CAC GCA TTG ATT TTT	GCC TGG AAT	AAG TGG ATA	GAT ATA AAA	CAA TTT GTA	TGG
H A L I F	A W N	K W I	D I K	Q F V	W
929	938	947	956	965	974
TAT ACA CCT CCA ACT	TTT ATG ATA	GCT GTT TTC	CTT CCA ATT	GTT GTC CTG	ATA
Y T P P T	F M I	A V F	L P I	V V L	I
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA	TTC CTG CCA	TGC TTG AGG	AAG ATA CTG	AAG ATT	AGA
F K S I L	F L P	C L R	K K I	L K I	R
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC	GTC ACC AAA	ATT AAC AAA	ACT GAG ATA	TGT TCC CAG	TTG
H G W E D	V T K	I N K	T E I	C S Q	L
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA	CAC ACA TTT	TTG TTC AAT	ATT GAT ATA	TTT TAT CAC	CAA
* N Y C L H	T F L	F N I	D I F	Y H Q	
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA	TTT GTT AAT	AAA ATG ATT	ATT CAA GGA	AAA AAA	AAA
H F K F V	F V N	K M I	I Q G	K K K	K

AAA AA 3'

-----

K

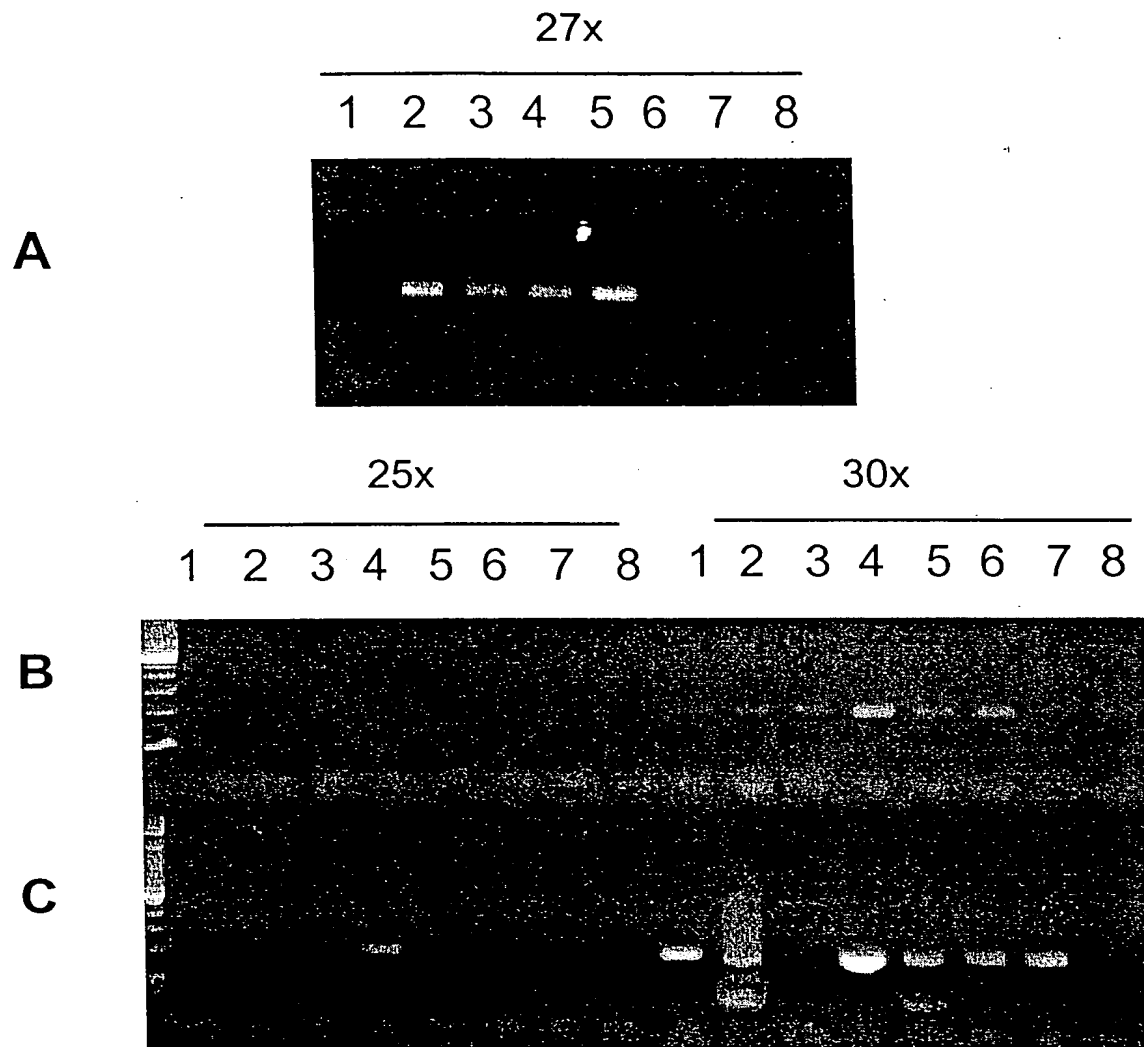
**FIG. 1B**



# FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG  
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT  
AAC AGC AAG 3'

**FIG. 2**



**Panels:**

**A**

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

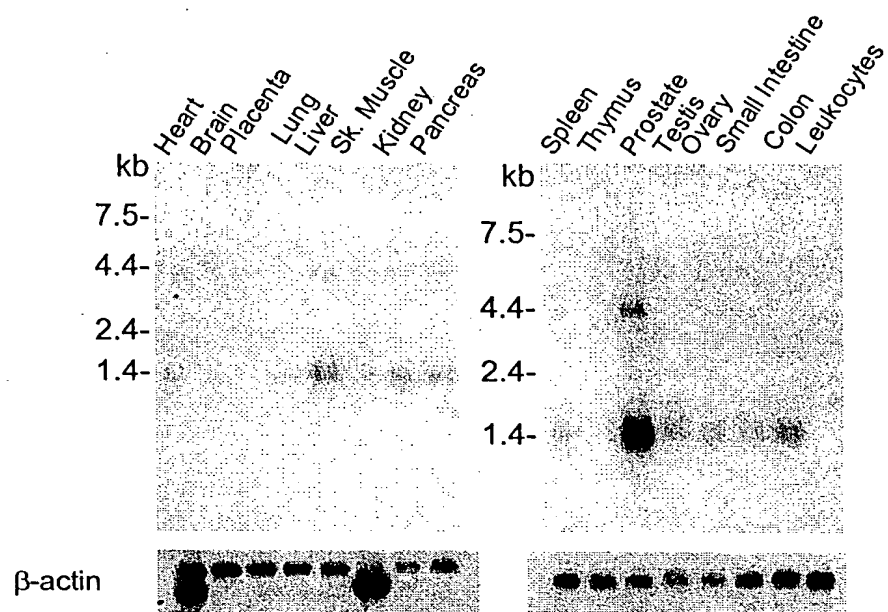
**B**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

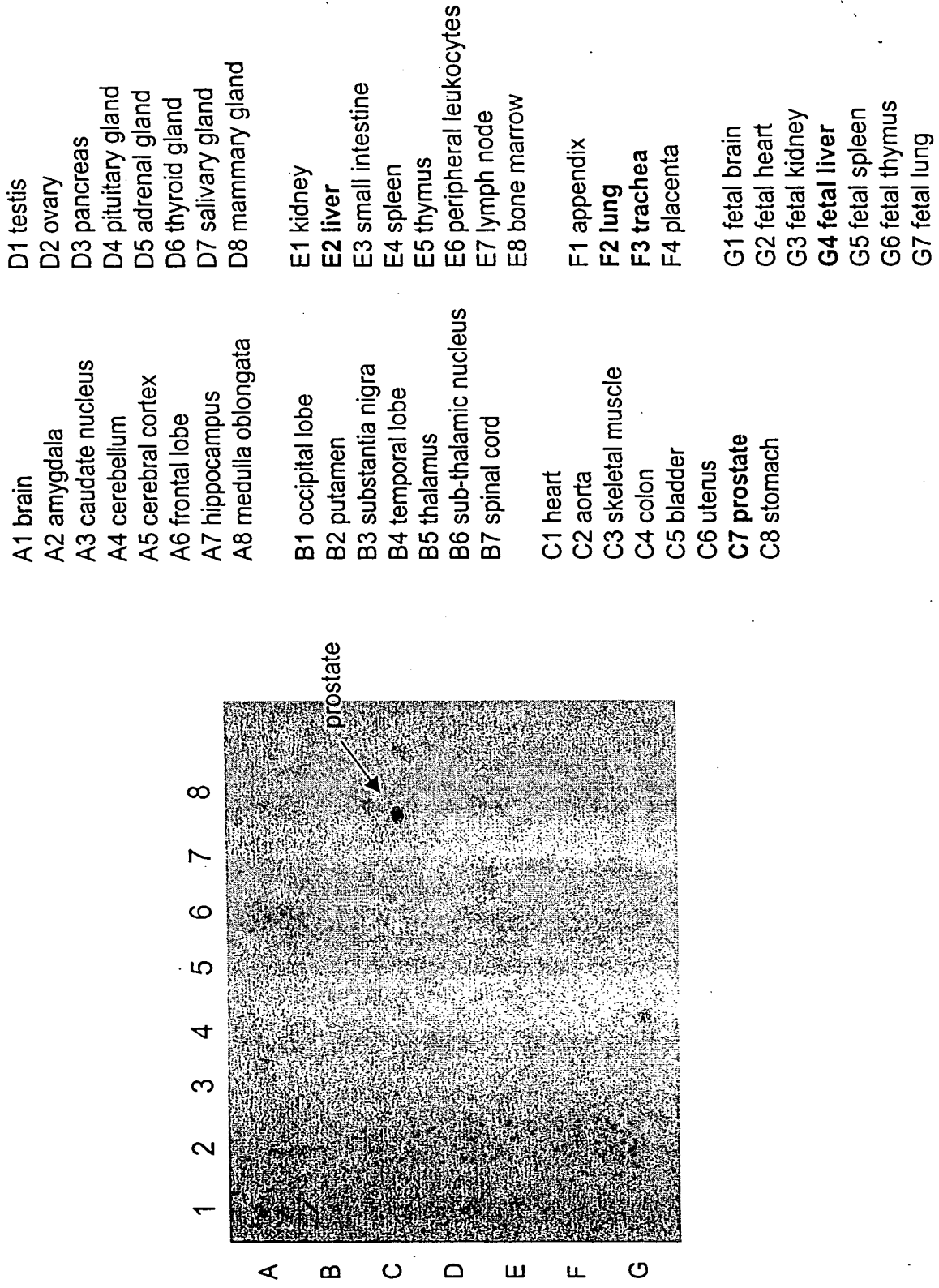
**C**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

**FIG. 3A**



# FIG. 3B



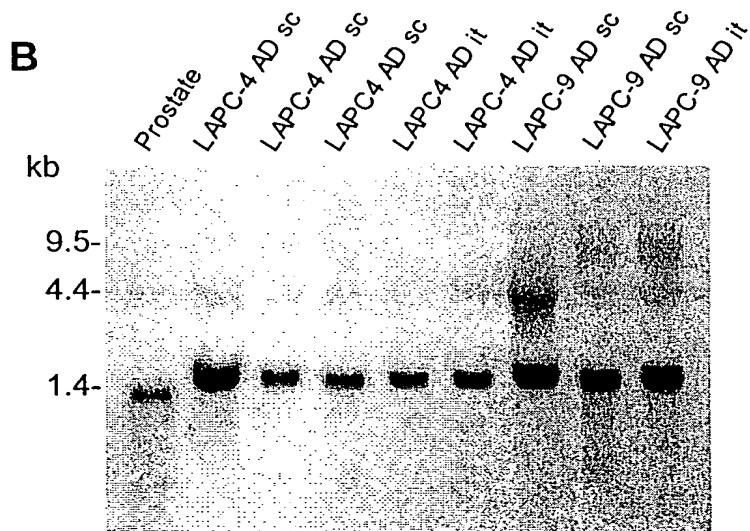
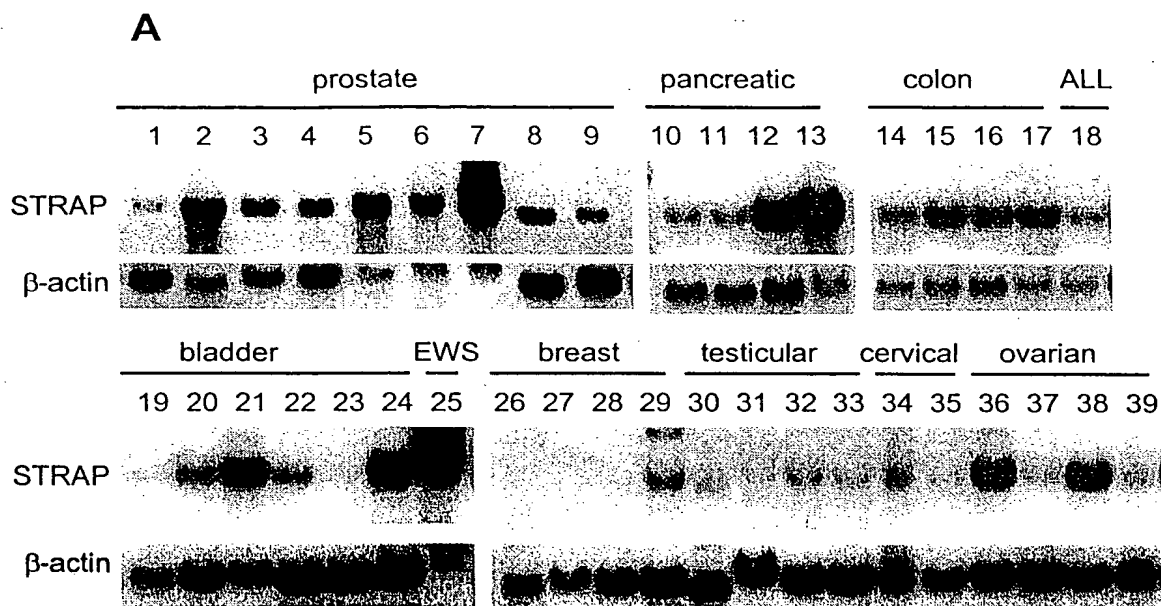


**FIG. 4**

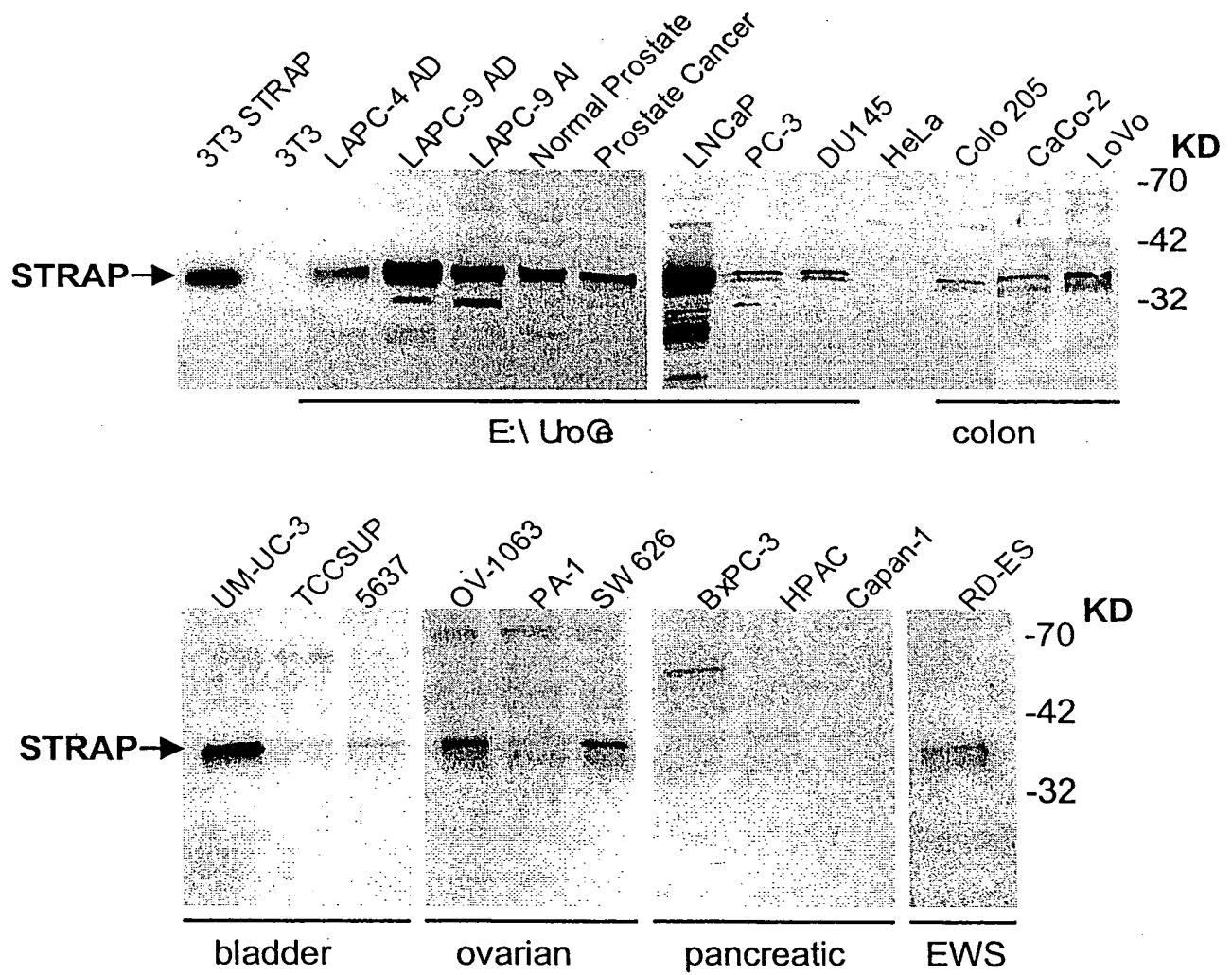
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AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC  
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTTTCCACA  
GTGGCACTTGCCAATTAATAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATT  
CACCCCTTAGCAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG  
TTTCCATCACTCTCTTGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA  
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT  
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT  
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT  
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG  
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT  
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT  
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCTTAGACATAAAATAAAGGCAT  
TAAAAATATCTTTGTTTTTTTTTTTTTGTGTTGTTGTTTTTGTGTTGTTGTTTTTGTGTTTTTTGAGATGAAGTCTCG  
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTTCAGGCGATTCT  
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTGTATTTTAGTA  
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC  
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAACTTGTTAGACAATTT  
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTCTTAAAAAAAATATTCTTTTACC  
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCCAGAAACAAAACTCTCTCCTTGAAA  
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT  
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT  
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAGATTCAAAGGACTAAA  
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT  
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGAAAGTATGC  
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTAATTTGTAGGTTTCAG  
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TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTCAACT  
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA  
ACGCAAACCTAGCTATTTGATTGTATTCCTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT  
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTGAGAAGTCGTATAAAAGAGGTGTTGTGAGAACACCGT  
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA  
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AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA  
CATTAGTCGCCTTCACAACCTGATAAAGATCACTGAAGTCAAATGATTTTTGCTATAATCTTCAATCTACCTATAT  
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TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG  
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TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCTGATATTTAAAGCATACTATT  
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG  
ATATGTTCCAGTTGTAAGATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA  
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# FIG. 5

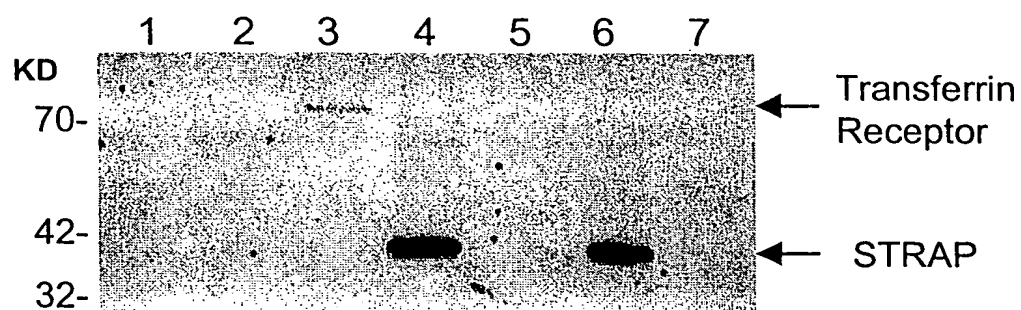


**FIG. 6**

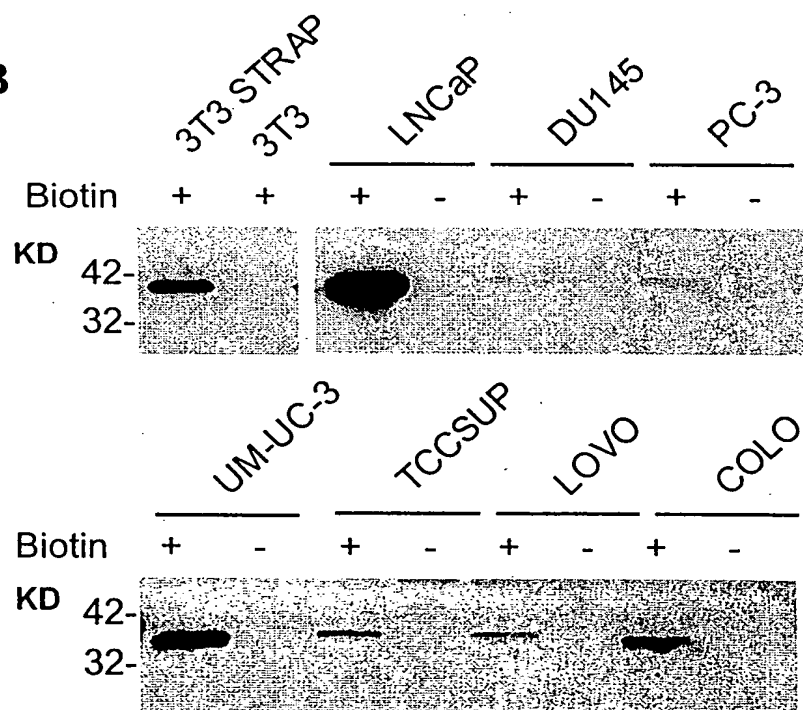


# FIG. 7

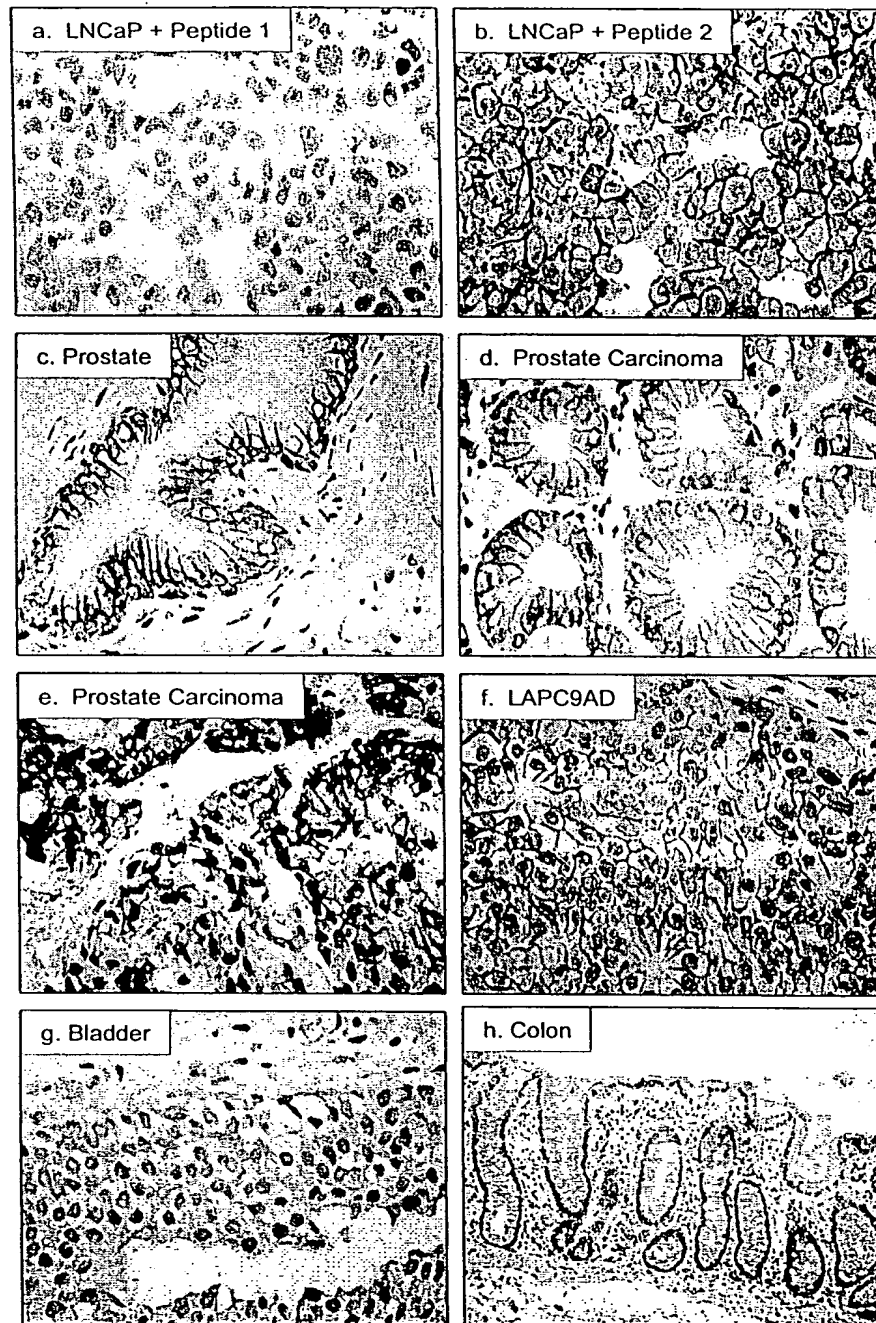
**A**



**B**



**FIG. 8**



# FIG. 9

```

      10      19      28      37      46      55
5' GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
   ---
   Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91      100      109
ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
   ---
   Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
   ---
   Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
   ---
   Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
   ---
   Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
   ---
   Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
   ---
   Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
   ---
   Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
   ---
   Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3'
   ---
   Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala

```

# FIG. 10

STRAP-2, AA508880 (NCI\_CGAP Pr6)

ggtcgacttttccctttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgactttttaca  
aaattccctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtagataccttgcagg  
tcttctggcagctgcttatcaactttattacggcaccaagttaggagatttccaccttggttggaaacctgggta  
cagtgtagaaaacagcttggattactaagtgtgttcttcgctatgggtccatgttgcctacagcctctgcttaccga  
tgagaaggtcagagagat

STRAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCTATTGACTCTACTTCTTTAAAAGCG  
GCTGCCCATTACATTCTCAGCTGTCTTGCAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC  
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt  
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt  
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacacctgggtgtacggtgggaagagattcctc  
agcccttcaaatctcagatgggtatcttctgcagcctacgtgttagggcttatcattccttgcactgtgctgggtga  
tcaagtttgtcctaataatcatgccatgtgtagacaacaccttacaaggatccgccagggtgggaaaggaactcaaa  
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaa

R80991 (placental EST)

ggccgcggcanccgctacgacctgggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg  
aaggaggaggtctggcggtggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggcgg  
tgacctcactgccgtccattgcaaactcgctcaactggagggagttcagcttcgttcagtcctcactgggctttgt  
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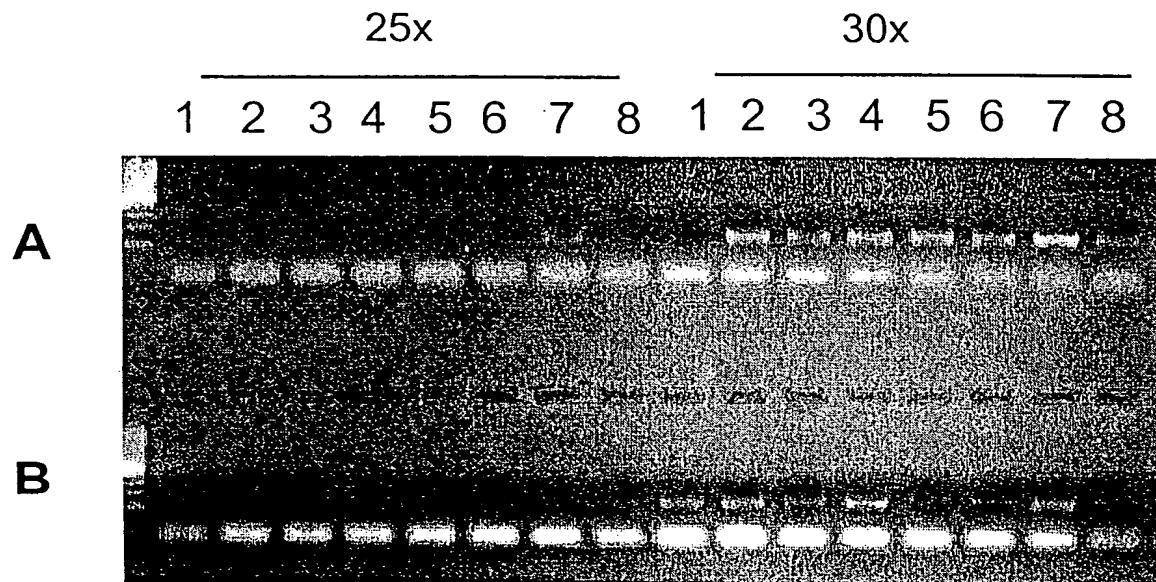


# FIG. 11A

```
STRAP-1 106 FYKIPILVINKVLPMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2 2 FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG
          ***** ** ** * ***** ** ** ** **
STRAP-1 166 LLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STRAP-2 62 LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
          ***** * *** ***** ** ** ***** ** * * ** * * * *
STRAP-1 226 GLAILALLAVTSIPSVDSLWREFHYIQSKLGIVSLLGTIHALIFAWNK
STRAP-2 122 SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
          * * ***** * ***** ** * * * * *
```

1	15 16	30 31	45 46	60 61	75 76	90
STRAP-1	MESRKOITNQBELWK	MKPRRNLEEDDYLHK	DTGETSMKRPVLLH	LHOTAHADEFDPCSE	LQHTQELFPQWHLPI	KIAAIIASLTFLYTL
STRAP-2	-----	-----	-----	-----	-----	-----
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
91	105 106	120 121	135 136	150 151	165 166	180
STRAP-1	LREVIHPLATSHQQY	FYKIPITLVNKKVLEPM	VSITLGLAVYDPGVI	AAIVQIDHNNTKYKRF	PHWLDKMWLTKRQVFG	DLSEFFFAVLHAIYSU
STRAP-2	-----D	FYKIPITLVNKKVLEPI	VAITLGLSVYDAGLL	AAIAQLYYSTKYRRE	FPWDETWLQCKRQVFG	DLSEFFFAVHVAVNSU
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
181	195 196	210 211	225 226	240 241	255 256	270
STRAP-1	SYPMRKSRVYKLVNWW	AYOOVQOONKEDAWIE	HDVWRMEIYVSIGIV	GLAIALGLAVTSIPS	VSDSLTWREHFHYIQS	KUGIVSDDLQCTIRAL
STRAP-2	CIPMRKSRERILFIDNN	AYOOVHANIENSWNE	EEVWRJEMWISFGIM	SLGLSLGLAVTSIPS	VSNALNWRRESFPIQS	TUGYVALLISTTHAVL
STRAP-3	-----	-----KKNPFST	SSAWLSDSVVALGIL	GPFLFVLDGITSIPS	VSNVAVNWRRESFEVQS	KUGYLTLLIQTIAHWI
STRAP-4	-----ATTWSTW	QSSRSWPXKSHLWVK	EEVWRMEIYLSLGIV	ALGTLSDGLAVTSIPS	IANSIANWRRESFEVQS	SLGFWAVVLSLTHLTI
821	285 286	300 301	315 316	330 331	345 346	360
STRAP-1	IFAWNKWIDIKQFVW	YTPPTFEMIAVELPIV	VLLTFKSILFIFCTIRK	KILKIRHGWEDVTKI	NKTEICSQL	339
STRAP-2	IYGNWKRA	-----	-----	-----	-----	173
STRAP-3	VYGGKRFSPSNLRW	YLPAAVVLGLIIPCT	VDVLIKFVLIMPVDPN	TLTRPQCWERNSKH	-----	128
STRAP-4	TYGWTRAFEEERYKE	YLPPTFTXTLLVPV	RSSWAKALFXLPICQ	P-----	-----	128

**FIG. 12**



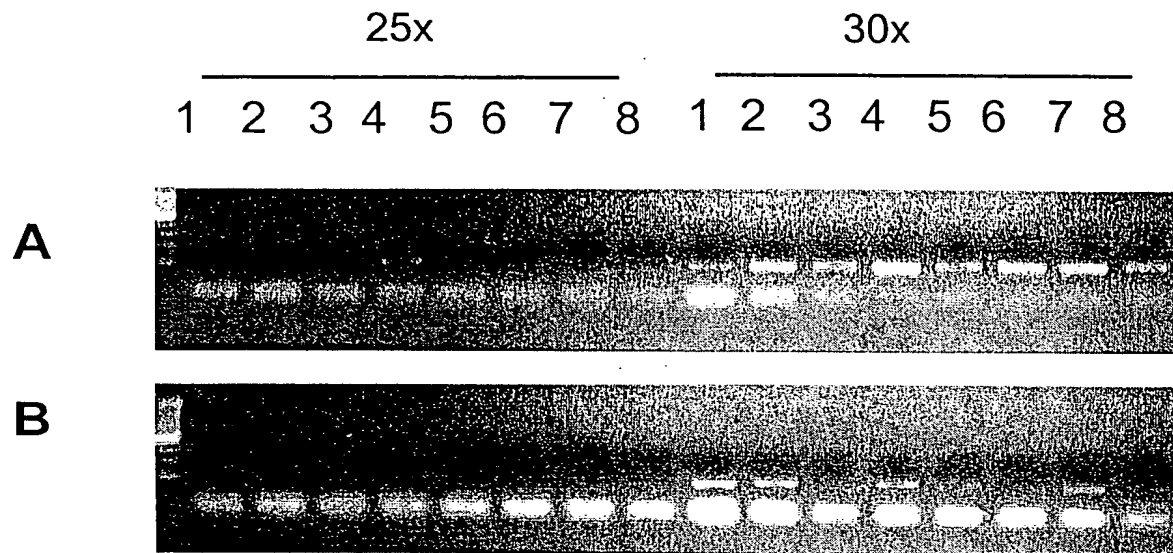
**A**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**B**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

**FIG. 13**



**A**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**B**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

**FIG.14**

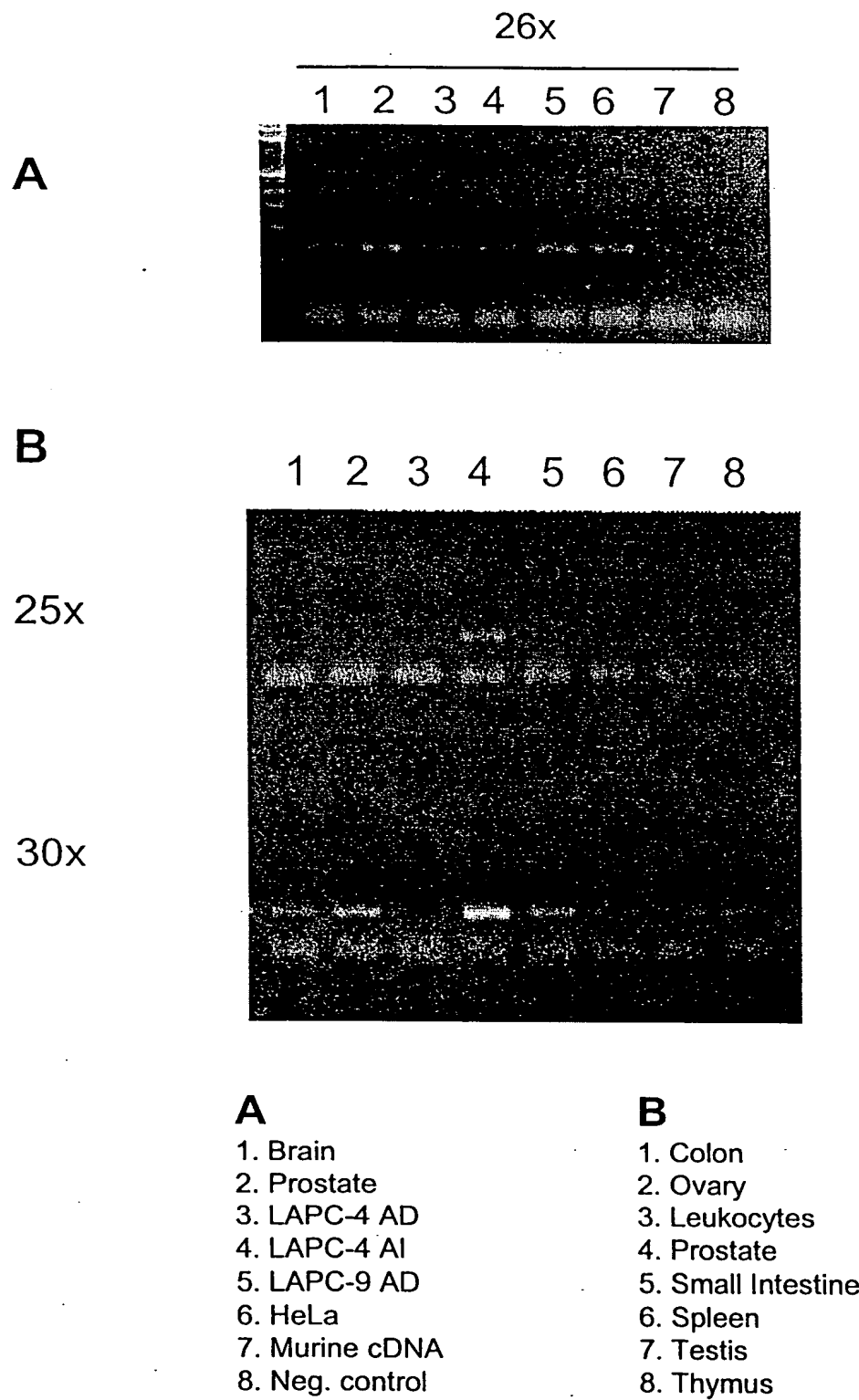
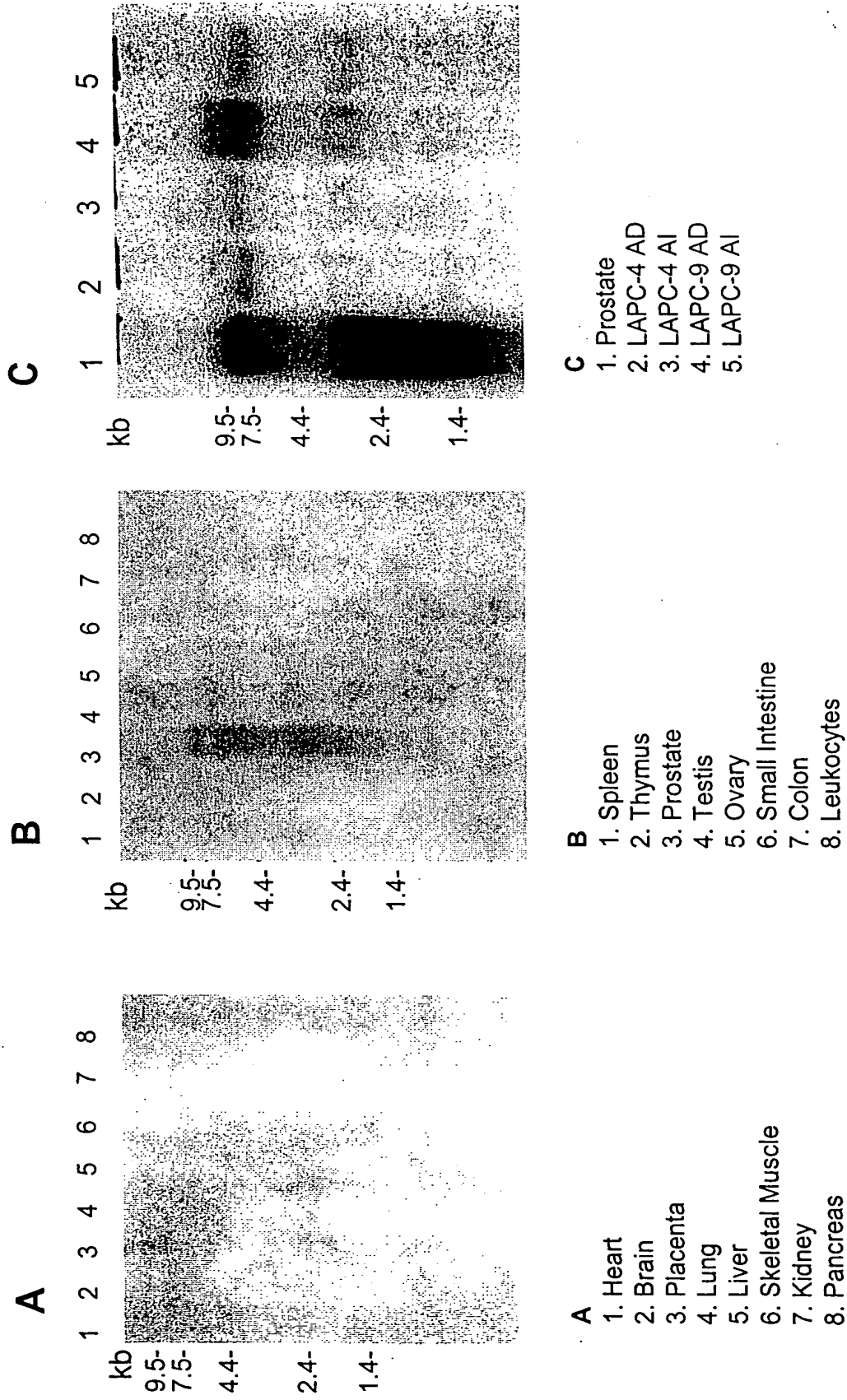
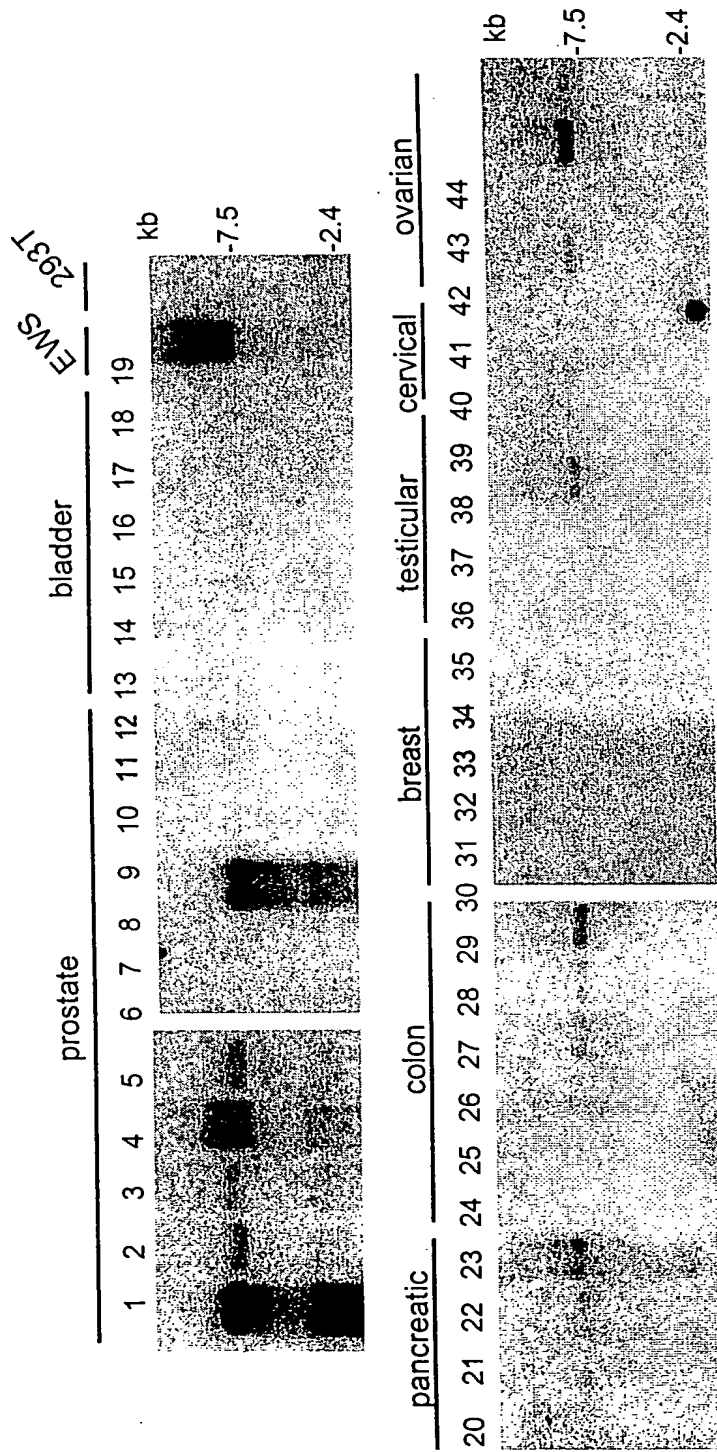


FIG. 15



# FIG. 16



- |               |                 |             |
|---------------|-----------------|-------------|
| 1. prostate   | 20. PANC-1      | 39. A431    |
| 2. LAPC-4 AD  | 21. BxPC-3      | 40. HeLa    |
| 3. LAPC-4 AI  | 22. HPAC        | 41. OV-1063 |
| 4. LAPC-9 AD  | 23. Capan-1     | 42. PA-1    |
| 5. LAPC-9 AI  | 24. LS180       | 43. SW626   |
| 6. TsuPr1     | 25. SK-CO-1     | 44. CAO-V-3 |
| 7. DU145      | 26. CaCo-2      |             |
| 8. LNCaP      | 27. LoVo        |             |
| 9. PC-3       | 28. T84         |             |
| 10. LAPC-4 CL | 29. Colo-205    |             |
| 11. PrEC      |                 |             |
|               | 30. BT-20       |             |
|               | 31. CAMA-1      |             |
|               | 32. DU4475      |             |
|               | 33. MCF-7       |             |
|               | 34. MDA-MB-435s |             |
|               | 35. NTERA-2     |             |
|               | 36. NCCIT       |             |
|               | 37. TERA-1      |             |
|               | 38. TERA-2      |             |

**FIG. 17**

**GDB Compreher**

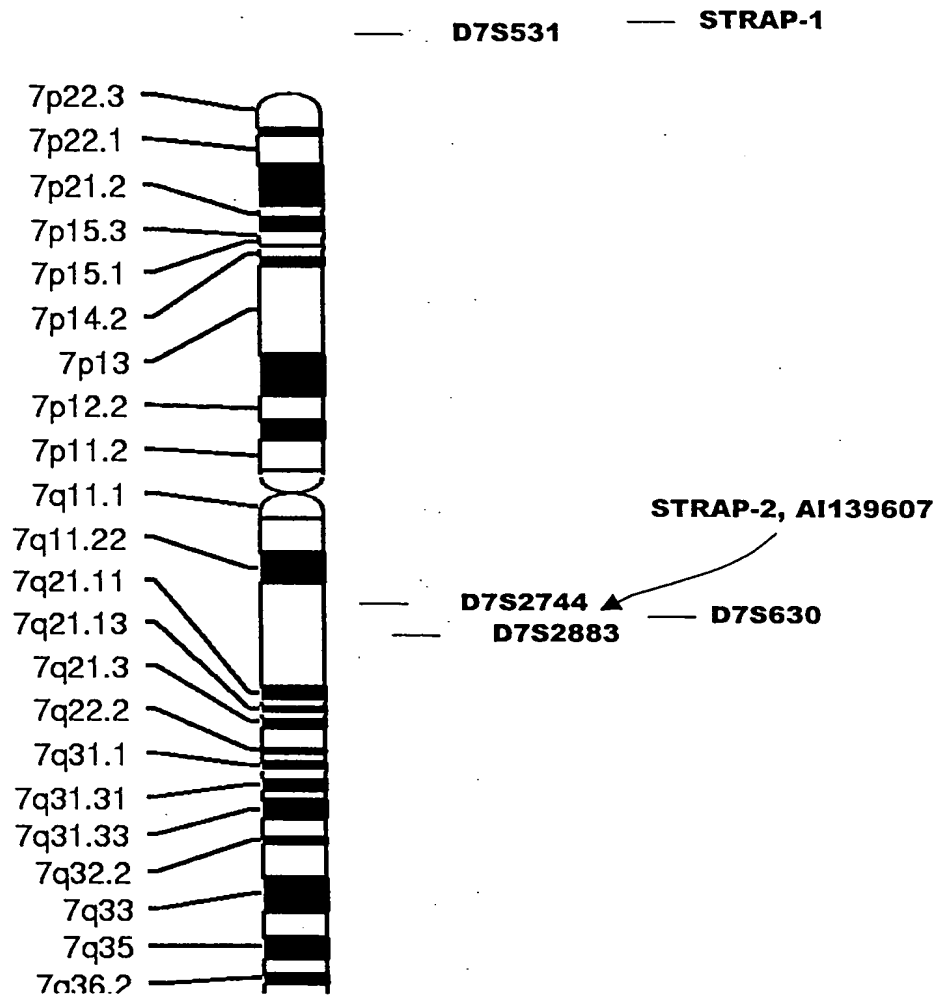
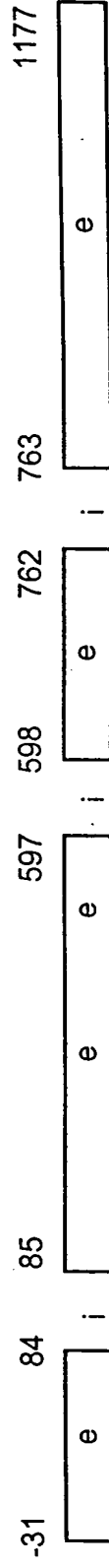
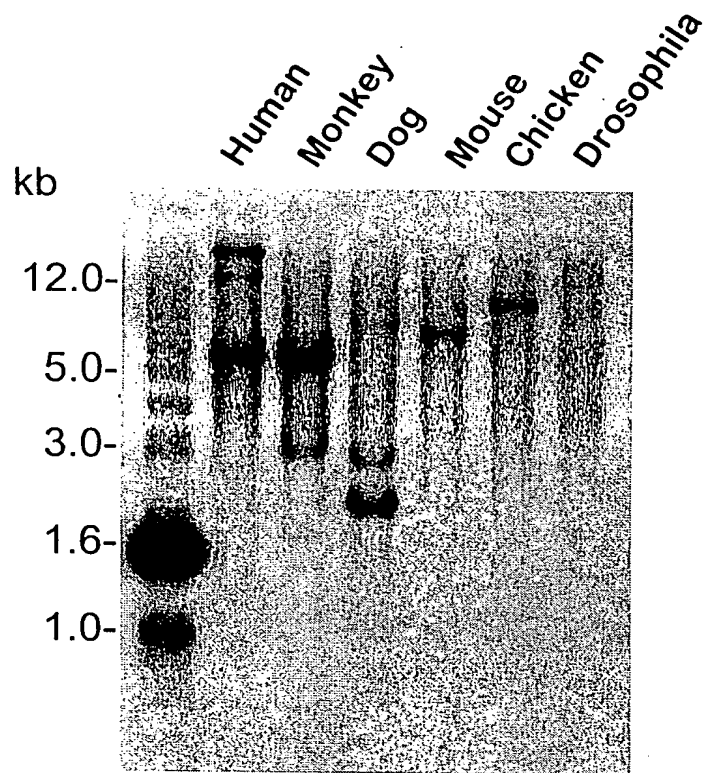




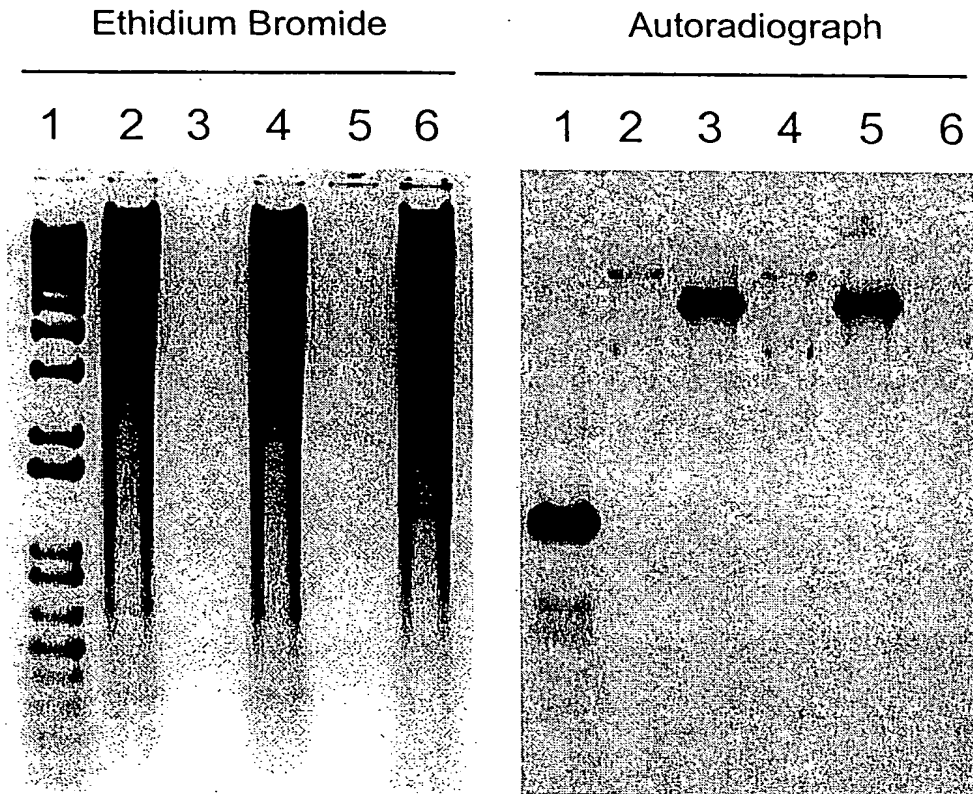
FIG. 18



**FIG. 19**



**FIG. 20**



**Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3